THAT WHICH IS CLAIMED:

1. An isolated nucleic acid molecule having a nucleotide sequence encoding a *Bt* toxin receptor, said sequence selected from the group consisting of:

a) a nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 5;

b) a nucleotide sequence having at least about 60 % identity to the nucleotide sequence of a);

c) a nucleotide sequence having at least about 70 % identity to the nucleotide sequence of a);

d) a nucleotide sequence having at least about 75 % identity to the nucleotide sequence of a);

e) a nucleotide sequence having at least about 85 % identity to the nucleotide sequence of a);

f) a nucleotide sequence having at least about 95 % identity to the nucleotide sequence of a);

g) a nucleotide sequence consisting of at least 22 contiguous nucleotides of the nucleotide sequence set forth in SEQ ID NO:1;

h) a nucleotide sequence consisting of at least about 15 contiguous nucleotides of the nucleotide sequence set forth in SEQ ID NO:3, or SEQ ID NO:5 ;

i) a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence of a); and

2. The nucleic acid molecule of claim 1, wherein said toxin is a Cry1A toxin.

3. The nucleic acid of claim 2, wherein said Cry1A toxin is a Cry1A(b) toxin.

4. An isolated polypeptide having the amino acid sequence selected from the group consisting of:

a) an amino acid sequence set forth in SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6;

b) an amino acid sequence having at least about 52% identity to the amino acid sequence set forth in SEQ ID NO: 2;

c) an amino acid sequence having at least about 60 % identity to the amino acid sequence of a);

d) an amino acid sequence having at least about 70 % identity to the amino acid sequence of a);

e) an amino acid sequence having at least about 75 % identity to an amino acid sequence of a);

f) an amino acid sequence having at least about 85 % identity to an amino acid sequence of a);

g) an amino acid sequence having at least about 95 % identity to an amino acid sequence of a);

h) an amino acid comprising at least about 15 contiguous residues of the amino acid nucleotide sequence of a);

i) an amino acid sequence encoded by a nucleotide sequence according to claim 1;

j) a variant of the amino acid sequence of a);

k) a fragment of the amino acid sequence of a); and

l) a fragment of the amino acid sequence of a) that binds *Bt* toxin.

5. A fusion polypeptide comprising the polypeptide of claim 4, and at least one polypeptide of interest.

6. The fusion polypeptide of claim 5, wherein said polypeptide of interest is a toxin receptor.

7. An expression cassette comprising a nucleotide sequence encoding the fusion polypeptide of claim 5, wherein said nucleotide sequence is operably linked to a promoter that drives expression in a cell of interest.

8. The expression cassette of claim 7 wherein said polypeptide of interest is a

toxin receptor.

9. An antibody preparation specific for the polypeptide of claim 4.

10. An expression cassette comprising at least one nucleotide sequence according to claim 1, wherein said nucleotide sequence is operably linked to a promoter that drives expression in a cell of interest.

11. The expression cassette of claim 10, wherein said cell of interest is an insect or mammalian cell.

12. The expression cassette of claim 10 wherein said cell of interest is a microorganism.

13. The expression cassette of claim 12 wherein said microorganism is yeast or bacteria.

14. A vector for delivery of a nucleotide sequence to a cell of interest, the vector comprising at least one nucleotide sequence according to claim 1.

15. A cell containing the vector of claim 14.

16. A transformed cell of interest having stably incorporated within its genome a nucleotide sequence selected from the group consisting of:

a) a nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 5;

b) a nucleotide sequence having at least about 60 % identity to the nucleotide sequence of a);

c) a nucleotide sequence having at least about 70 % identity to the nucleotide sequence of a);

d) a nucleotide sequence having at least about 75 % identity to the

nucleotide sequence of a);

e) a nucleotide sequence having at least about 85 % identity to the nucleotide sequence of a);

f) a nucleotide sequence having at least about 95 % identity to the nucleotide sequence of a);

g) a nucleotide sequence consisting of at least 22 contiguous nucleotides of the nucleotide sequence set forth in SEQ ID NO:1;

h) a nucleotide sequence consisting of at least about 15 contiguous nucleotides of the nucleotide sequence set forth in SEQ ID NO:3, or SEQ ID NO:5 ;

i) a nucleotide sequence that hybridizes under stringent conditions to the nucleotide sequence of a); and

17. The transformed cell of claim 16 , wherein said cell is a plant cell.

18. The transformed cell of claim 17, wherein said plant cell is monocotyledonous.

19. A method for screening for ligands that bind *Bt* toxin receptor, said method comprising:

i) providing at least one *Bt* toxin receptor polypeptide according to claim 4;

ii) contacting said polypeptide with a sample and a control ligand under conditions promoting binding; and

iii) determining binding characteristics of said sample ligand, relative to said control ligand.

20. A method for screening for ligands that bind *Bt* toxin receptor, said method comprising:

i) providing at least one *Bt* toxin receptor polypeptide having the amino acid sequence selected from the group consisting of a, b, c, d, e, f, g, h , i, and j of claim 4 in cells expressing said polypeptide wherein said polypyptide comprises a toxin

binding domain ;

ii) contacting said cells with a sample and a control ligand under conditions promoting binding; and

iii) determining binding characteristics of said sample ligand, relative to said control ligand.

21. The method of claim 20 wherein said toxin is a Cry1A toxin.

22. A method for screening for toxins that bind Bt toxin receptor, said method comprising the steps of claim 20, further comprising determining viability of said cells contacted with a sample ligand relative to said cells contacted with a control ligand.

23. The method of claim 20, wherein said sample ligand is a chimeric polypeptide comprising at least one primary polypeptide that binds a polypeptide having the amino acid sequence selected from the group consisting of:

a) an amino acid sequence set forth in SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6;

b) an amino acid sequence having at least about 52% identity to the amino acid sequence set forth in SEQ ID NO: 2;

c) an amino acid sequence having at least about 60 % identity to the amino acid sequence of a);

d) an amino acid sequence having at least about 70 % identity to the amino acid sequence of a);

e) an amino acid sequence having at least about 75 % identity to an amino acid sequence of a);

f) an amino acid sequence having at least about 85 % identity to an amino acid sequence of a);

g) an amino acid sequence having at least about 95 % identity to an amino acid sequence of a);

h) an amino acid comprising at least about 15 contiguous residues of the amino acid nucleotide sequence of a);

i) an amino acid sequence encoded by a nucleotide sequence having at least about 60 % identity to the nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 5; and

j) a variant of the amino acid sequence of a).

24. The method of claims 21, wherein said sample ligand is a chimeric polypeptide comprising at least one primary polypeptide that binds a polypeptide having the amino acid sequence selected from the group consisting of:

a) an amino acid sequence set forth in SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6;

b) an amino acid sequence having at least about 52% identity to the amino acid sequence set forth in SEQ ID NO: 2;

c) an amino acid sequence having at least about 60 % identity to the amino acid sequence of a);

d) an amino acid sequence having at least about 70 % identity to the amino acid sequence of a);

e) an amino acid sequence having at least about 75 % identity to an amino acid sequence of a);

f) an amino acid sequence having at least about 85 % identity to an amino acid sequence of a);

g) an amino acid sequence having at least about 95 % identity to an amino acid sequence of a);

h) an amino acid comprising at least about 15 contiguous residues of the amino acid nucleotide sequence of a);

i) an amino acid sequence encoded by a nucleotide sequence having at least about 60 % identity to the nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 5; and

j) a variant of the amino acid sequence of a).

25. The method of claims 22, wherein said sample ligand is a chimeric polypeptide comprising at least one primary polypeptide that binds a polypeptide having

the amino acid sequence selected from the group consisting of:

a) an amino acid sequence set forth in SEQ ID NO: 2, SEQ ID NO: 4, or SEQ ID NO: 6;

b) an amino acid sequence having at least about 52% identity to the amino acid sequence set forth in SEQ ID NO: 2;

c) an amino acid sequence having at least about 60 % identity to the amino acid sequence of a);

d) an amino acid sequence having at least about 70 % identity to the amino acid sequence of a);

e) an amino acid sequence having at least about 75 % identity to an amino acid sequence of a);

f) an amino acid sequence having at least about 85 % identity to an amino acid sequence of a);

g) an amino acid sequence having at least about 95 % identity to an amino acid sequence of a);

h) an amino acid comprising at least about 15 contiguous residues of the amino acid nucleotide sequence of a);

i) an amino acid sequence encoded by a nucleotide sequence having at least about 60 % identity to the nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 3 or SEQ ID NO: 5; and

j) a variant of the amino acid sequence of a).

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